Amendment to the Specification:

Please amend the paragraph beginning on page 3, line 32 and continuing to page 4, line 4 as follows:

Assume there are a number of monitored signals ~~(s_1, s_2, s_3, ..., s_n),~~ (S_1, S_2,S_3, ..., S_n), for which one needs to have an indicator for the presence of artifacts in every signal. The process starts by running off-line correlation testing among recorded banks of these signals. ECG/EEG signal database sources are publicly available and can be easily obtained. The resulting correlation matrix gives an indicator of the cross dependency between every pair of these signals and would be of the form:

$$\begin{bmatrix} r_{11} & \cdots & r_{1n} \\ \vdots & & \vdots \\ r_{n1} & \cdots & r_{nn} \end{bmatrix} \qquad (1)$$

where r_{11} is the autocorrelation of signal ~~s_1~~ S_1 with itself (r_{11}=1) and r_{1n} is the cross correlation between signals ~~s_1~~ S_1 and ~~s_n~~ S_n. These cross correlation values are needed for the statistical analysis as shown in FIG 1. The National Institutes of Health have developed such a database from which these cross-correlation values can be obtained.

Please amend the paragraph beginning on page 5, line 15 and continuing to page 5, line 13 as follows:

Based on prior testing of the monitored signals under study ~~(s_1, s_2, s_3, ..., s_n)~~ (S_1, S_2,S_3, ..., S_n) as stored in the databanks, and identifying correlated signals as in equation (1), we set a certain threshold to determine the accepted level of correlation (*e.g.*, reject any correlation factor r_{ij} less than 40%). We repeat the same experiment (which results in a different correlation matrix) for every clinical condition under examination (*e.g.*, angina, bleeding, brain injury, pulmonary edema, cord compression, metabolic coma, respiratory failure, ..., etc). Each clinical condition will have its own correlation matrix, which describes the success of having

any two signals pass hypothesis testing when compared against each other. For example, as shown in FIG 1, signals ~~s_1~~ S_1 and ~~s_2~~ S_2 have a certain correlation factor r_{12}, and a certain range of p-values (*e.g.*, $p_{minAngina}$, $p_{maxAngina}$) in the case of angina, which is different from the case of respiratory failure. The closer the currently produced values from the normal range, the higher the corresponding weight it has. This is measured by assigning more weight to the p values closer to the nominal ones. For example,

On page 5, line 14, please delete current Equation (2) and replace it with the following corrected Equation (2):

$$p_{i,j} = \frac{p_{i,j} - 0.5\left(p_{i,j\max Angina} + p_{i,j\min Angina}\right)}{\left(p_{i,j\max Angina} - p_{i,j\min Angina}\right)} \times c_{i,j} \qquad (2)$$